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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                 Copyright
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- protein search, using sw model OM protein November 12, 2003, 15:41:34; Search time 9.84282 Seconds (without alignments) 640.499 Million cell updates/sec Run on:

US-09-963-347B-2 769 1 MGCPRMFPFALLYVLSVSFR......KKRRKRKYTTNKCLEQVSQL 149 Title: Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

328717 Total number of hits satisfying chosen parameters:

328717 segs, 42310858 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Patents AA:* Issued Database :

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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 2. Appli	4		, ,	Sequence 2, Appli	9	7	7	7	574	46. At	46,	4	46,	46,	46	46,	46,	53,	53,	53,	23	53	53	53	4	Sequence 9, Appli
SUMMARIES	QI	US-09-852-391-2	US-09-328-352-6455	US-08-993-228-10	US-09-627-986-1	US-09-213-053-2	US-09-417-485D-6	US-08-446-908-2	US-08-231-205A-2	US-08-871-161-2	US-09-328-352-5747	US-08-286-889-46	US-08-485-618-46	US-08-362-652-46	US-08-605-672-46	US-08-482-293A-46	US-08-943-363-46	US-09-193-043-46	US-09-688-307A-46	US-08-485-618-53	US-08-362-652-53	US-08-605-672-53	US-08-482-293A-53	US-08-943-363-53	US-09-193-043-53	US-09-688-307A-53	US-09-356-952-4	US-08-430-286A-9
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	Score	707	81.5	73	72.5	71.5	71.5	71	71	71	71	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	69	89
	Result No.	7	7	e	4	Ŋ	9	7	æ	σ	10	11	12	13	14	15	16	17	18	61	20	21	22	23	24	25	26	27

Sequence 2, Appli	Sequence 317, App	Sequence 27368, A	Sequence 21, Appl	Sequence 21, Appl	12,	Sequence 14, Appl	Sequence 12, Appl	14,	12,	14,	9	Sequence 6, Appli	10,	2, A	Sequence 10, Appl	Sequence 10, Appl	Sequence 10, Appl
US-09-308-375-2	US-09-198-452A-317	US-09-252-991A-27368	US-07-937-609-21	US-08-029-170-21	US-08-220-151-12	US-08-220-151-14	US-08-413-118-12	US-08-413-118-14	US-08-473-446-12	US-08-473-446-14	US-09-213-053-6	PCT-US92-00282-6	US-08-430-286A-10	US-07-725-083-2	US-08-669-286-10	US-09-469-253-10	US-09-642-146-10
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89 1	67.5	67	63	67	67	67	67	63	63	67	67	66.5	99	99	99	99	99
8 6	0.0	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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TEFNNIVSCSNRPHCLTEIQSLTFNPNRRVRSLAKEMFAMKTKAALAIWCPGYSETQINA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MFPFALLYVLSVSFRKIFILQLVGLVLTYDFTNCDFEKIKAAYLSTISKDLITYMSGTKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 707; DB 4; Length 159;
Pred. No. 2.5e-75;
); Mismatches 5; Indels
                             Sequence 2, Application US/09852391
Patent No. 655520
GENERAL INFORMATION:
APPLICANT: Sims, John
APPLICANT: Lyman, Stewart
APPLICANT: Armstrong, Allison
APPLICANT: Human TSLP DNA and Polypeptides
FILE REFERENCE: 03260.0087-00304/2881-WO
CURRENT APPLICATION NUMBER: US/09/852,391
CURRENT FILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENT Ver. 2.0
SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                            91.9%; Score ... 5e-7
96.5%; Pred. No. 2.5e-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 96.5
Matches 139; Conservative
                                                                                                                                                                                                                                                                                                                                          LENGTH: 159
TYPE: PRT
ORGANISM: Homo sapiens
RESULT 1
US-09-852-391-2
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RESULT 2 g

US-09-328-352-6455
; Sequence 6455, Application US/09328352
; Batent No. 6562588
; GENERAL NO. 6562258
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352

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GenCore version 5.1.6
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- nucleic search, using sw model OM nucleic

November 12, 2003, 15:45:54; Search time 56 Seconds (without alignments) 3783.284 Million cell updates/sec Run on:

US-09-963-347B-3 Title:

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IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

569978 seqs, 220691566 residues Searched:

Total number of hits satisfying chosen parameters:

1139956

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents NA:* Database :

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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:* **αω4πο**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMADIES

	Description	Sequence 1, Appli	Sequence 1, Appli	ન	2, 7	42,	524,	9 1,	Sequence 1, Appli	456	Sequence 2, Appli	н	32	'n	5		ហ	'n	-	~	ĭ	'n	디	41,	Sequence 6, Appli	11	ä	Sequence 1, Appli
SUMMARIES	ID	US-09-852-391-1	US-09-198-452A-1	US-08-916-421B-1	PCT-US94-09752-2	US+09-288-143-42	US-09-328-352-524	US-09-557-884-1	US-09-643-990A-1	US-09-252-991A-14566	US-09-103-840A-2	US-09-103-840A-1	US-09-404-879A-321	US-08-026-145-5	US-08-446-646-10	US-08-446-646-4	US-08-817-707-5	US-09-734-675-3	US-08-916-421B-1	US-09-557-884-1	US-09-643-990A-1	US-07-885-089B-5	US-08-858-207A-153	US-09-671-317-412	US-09-481-049-6	US-09-356-806-112	US-09-356-806-114	US-08-697-954-1
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o)	Query Match	100.0	7.2	7.0	9.9	6.5	6.5	6.5		6.3	6.3	6.3	6.3	6.2	6.2	6.2	6.2	6.2	6.2	6.2	6.2	6.1	6.1	6.1	6.1	6.1	6.1	6.1
	Score	480	34.4	33.4	31.8	31	31	31	31	30.4	30.4	30.4	30.2	30	30	30	29.6	29.6	29.6	29.6	29.6	29.4	29.4	29.5	29.5	29.5	29.3	29.3
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28 29.2 6.1 580073 4 US-08-545-528D-1 c 29 29 6.0 2097 3 US-08-655-346-3 c 31 29 6.0 2097 3 US-08-655-346-3 c 32 29 6.0 2097 4 US-09-727-169-3 c 34 29 6.0 2097 4 US-09-727-169-3 c 34 29 6.0 2097 4 US-09-727-169-3 c 35 29 6.0 2097 5 VC-0896-3 c 37 29 6.0 2475 4 US-09-134-001C-1003 c 37 29 6.0 2475 3 US-09-134-001C-1003 c 38 29 6.0 2475 3 US-09-134-001C-1003 c 40 29 6.0 2475 4 US-09-726-968-1 c 40 29 6.0 2475 4 US-09-727-169-1 c 41 29 6.0 2475 4 US-09-737-169-1 c 42 29 6.0 2475 4 US-09-377-169-1 c 43 28 6.0 2475 4 US-09-377-169-1 c 44 28 6.0 2475 4 US-09-377-169-1 c 45 29 6.0 2475 4 US-09-377-169-1 c 47 29 6.0 2475 4 US-09-377-169-1 c 48 28 6.0 2475 4 US-09-377-169-1 c 49 29 6.0 2475 4 US-09-377-169-1 c 49 29 6.0 2475 4 US-09-377-169-1 c 49 29 6.0 2475 4 US-09-377-169-1 c 49 28 6.0 2475 4 US-09-377-169-1 c 49 28 6.0 2475 4 US-09-377-169-1 c 49 29 6.0 2475 4 US-09-377-169-1 c 49 28 6.0 2475 4 US-09-377-169-1	Sequence 1, Appli	Sequence 3, Appli	Sequence 1003, Ap	Sequence 1, Appli	'n	Sequence 64, Appl												
28 29.2 6.1 580073 31 29 6.0 2097 32 29 6.0 2097 33 29 6.0 2097 34 29 6.0 2097 35 29 6.0 2475 36 29 6.0 2475 37 29 6.0 2475 38 29 6.0 2475 40 29 6.0 2475 41 29 6.0 2475 42 29 6.0 2475 44 28.8 6.0 3014 500 500 500 500 500 500 500 500 500 500	US-08-545-528D-1	US-08-655-345-3	US-09-183-275-3	US-09-727-169-3	US-09-579-766A-3	US-09-726-968-3	PCT-US96-08407-3	US-09-134-001C-1003	US-08-655-345-1	US-09-183-275-1	US-09-727-169-1	US-09-579-766A-1	US-09-726-968-1	PCT-US96-08407-1	US-09-429-093-1	US-08-913-374-1	US-09-012-669F-2	US-08-084-718-64
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28 28 28 28 28 28 28 28 28 28 28 28 28 2	6.1	6.0	6.0	0.9	0.9	0.9	6.0	6.0	9	6.0	6.0	6.0	6.0	9.0	0.9	0.9	6.0	6.0
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ALIGNMENTS

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61 CAACTIGTAGGGCTGGTGTTAACTTAAGGACTTCACTAACTGTGACTTTGAGAAGATTAAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     320 GCAGCCTATCTCAGTACTATTCTAAAGACCTGATTACATATATGAGTGGGACCAAAAGT 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 ACCGAGTTÇAACAACAÇÇGTCTCTTGTAGCAATCGGCCACATTGCCTTACTGAAATCCAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         380 ACCGAGITICAACAACACCGICICITIGIAGCAATCGGCCACATGGCCTTACTGAAATCCAG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 AGCCTAACCTTCAATCCCACCGCCGCTGCGTCGCTCGCCAAGGAAATGTTCGCCATG 300
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              Sequence 1, Application US/09852391
Patent No. 655528
GENERAL INFORMATION:
APPLICANT: Sims, John
APPLICANT: Lyman, Stewart
APPLICANT: Armetrong, Allison
CURRENT APPLICATION NUMBER: US/09/852,391
CURRENT FILIG DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 60/108,452
PRIOR APPLICATION NUMBER: 60/108,452
PRIOR APPLICATION NUMBER: 00/108,452
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match (100.0%; Score 480; DB 4; I Best Local Similarity 100.0%; Pred No. 2.9e-148; Matches 480; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Homo sapiens
US-09-852-391-1
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1
LENGTH: 743
US-09-852-391-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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NAME/KEY: misc feature
LOCATION: (22501)..(24000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (24001)..(25500)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (25501)..(27000)
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LOCATION: (25501)..(27000)
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NAME/KEY: misc feature
LOCATION: (31501)..(313000)
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LOCATION: (555001). (570000)
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LOCATION: (450001)...(465000)
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LOCATION: (40501)..(420000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (57001)..(585000)
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LOCATION: (480001)..(495000)
OTHER INFORMATION: n=a or c or g or
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OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc feature
LOCATION: (510001)..(525000)
OTHER INFORMATION: n=a or c or g or
                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09198452A

Sequence 1, Application US/09198452A

GENERAL INFORMATION:
APPLICANT: Griffais, R.

APPLICANT: Griffais, R.

APPLICANT: Griffais, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve

TITLE OF INVENTION: and treatment of infection

TITLE OF INVENTION: 4053-999

CURRENT APPLICATION NUMBER: 1998-11-24

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 1

LENGTH: 1230025
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LOCATION: (105001)..(120000)

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OTHER INFORMATION: n=a or c or g or t
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LOCATION: (120001)..(135000)
OTHER INFORMATION: n=a or c or g or
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OTHER INFORMATION: n=a or c or g or t
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OTHER INFORMATION: n=a or c or g or
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OTHER INFORMATION: n=a or c or g.
MMB/KEY: misc feature
LOCATION: (15001)...(3000)
OTHER INFORMATION: n=a or c or g.
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US-09-198-452A-1/c
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November 12, 2003, 15:41:34; Search time 10.5034 Seconds (without alignments) 640.499 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                  OM protein - protein search, using sw model
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Issued Patents AA:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 2, Appli			46,		46,	46,	46,	46,	46,	53,	53,	53,	53,	Seguence 53, Appl	53,	53	10		ģ	ď	ď	٦,	7,	4	Sequence 2, Appli	273	
SUMMARIES	ID	US-09-852-391-2	US-09-328-352-6455	US-08-286-889-46	US-08-485-618-46	US-08-362-652-46	-605-	28	US-08-943-363-46	US-09-193-043-46	US-09-688-307A-46	US-08-485-618-53	US-08-362-652-53	0	US-08-482-293A-53	US-08-943-363-53	US-09-193-043-53	889-60-	US-08-993-228-10	US-09-198-452A-415	PCT-US92-00282-6	US-08-949-588-2	US-09-213-053-2	US-09-627-986-1	US-09-180-827-7	US-09-356-952-4	US-09-308-375-2	US-09-252-991A-27368	
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	Score	823	74.5	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	71	σ	69.5	g	α	68	89	69	67	
	Result No.		7	m	4	5	9	7	83	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	

4, (Sequence 2, Appli	Sequence 2, Appli	Sequence 53, Appl		Sequence 53, Appl	5747	Sequence 292, App	5, 7	4	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	7	Sequence 2, Appli	25,	Sequence 25, Appl	25,
US-09-328-352-4934	US-08~673-814-2	US-09-115-824-2	US-08-975-762-53	US-09-295-028-53	US-09-106-582-53	US-09-328-352-5747	US-09-170-496D-292	US-08-746-111-5	US-08-946-026-4	US-08-948-276-4	US-08-344-695-2	US-08-446-908-2	US-08-231-205A-2	US-08-871-161-2	US-08-361-920-25	US-08-479-939-25	US-08-483-432-25
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ALIGNMENTS

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                                                                                             APPLICANT: Sime, John
APPLICANT: Sime, John
APPLICANT: Lyman, Stewart
APPLICANT: Armstrong, Allison
APPLICANT: McKenna, Hilary
TITLE OF INVENTION: Human TSLP DNA and Polypeptides
FILE REFERENCE: 03260,0087-00304/2881-WO
CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 60/108,452
PRIOR APPLICATION NUMBER: 60/108,452
PRIOR APPLICATION NUMBER: 1998-11-13
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
                      Sequence 2, Application US/09852391; Patent No. 6555520; GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 159; Conservative
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US-09-852-391-2
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61 TEFNNTVSCSNRPHCLTEIQSLTFNPTAGCASLAKEMFAMKTKAALAIWCPGYSETQINA 120 61 TEFNNTVSCSNRPHCLTEIQSLTFNPTAGCASLAKEMFAMKTKAALAIWCPGYSETQINA 120 1 MFPFALLYVLSVSFRKIFILQLVGLVLTYDFTNCDFEKIKAAYLSTISKDLITYMSGTKS 60 121 TQAMKKRRKKVTTNKCLEQVSQLQGLWRRFNRPLLKQQ 159 121 TOAMKKRRKKVTTNKCLEOVSOLOGLWRRFNRPLLKOO 159 Sequence 6455, Application US/09328352 Patent No. 6562958 RESULT 2 US-09-328-352-6455 g 셤 õ ð ద

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0; Gaps

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Patent No. 6562959
GENERAL INCOMMATION:
GENERAL INCOMMATION:
APPLICANT: GATY L. Breton et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER;
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352

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(without alignments)
640.499 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. 1: / cgn2_6/ptodata/2/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:*

Database

SUMMARIES

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7	73	10.8	1155	Н	9	46,
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17	73	10.8		N	US-08-993-228-10	10
18	69.5	10.3	531	ഗ	PCT-US92-00282-6	ý
19	68	10.1	1589	m	US-09-356-952-4	4,
20	63	9.9	2285	4	US-09-308-375-2	'n
21	99	8.6	366	ሎ	US-08-975-762-53	23
22	99			m	US-09-295-028-53	53
23	99	9.8	366	4	US-09-106-582-53	53
24	65.5	6.3	321	4	US-08-948-276-4	4
25	S	7.6	465	4	US-09-627-986-1	ť
26		9.6	154	4	US-09-252-991A-27368	
27	65	9.6	589	Н	US-07-668-648-6	

Sequence 46, Application US/08286889
Patent No. 5470953
GENERAL INFORMATION, W. Mich
APPLICANT: Gallatin, W. Mich
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTYON: No. 5470953el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:

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Sequence 4455, Ap
Sequence 29, Appli
Sequence 15, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3795, Ap
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APPLICANT: Lyman, Stewart
APPLICANT: Armstrong, Jalison
APPLICANT: Hillison
APPLICANT: Hillison
APPLICANT: Armstrong, Hillison
APPLICANT: 10360,0087-00304/2881-WO
FILE REFERENCE: 03260,0087-00304/2881-WO
CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 60/108,452
PRIOR APPLICATION NUMBER: 60/108,452
NUMBER OF ERQ ID NOS: 5
NUMBER OF ERQ ID NOS: 5
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US-09-066-046-29
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US-08-029-170-17
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US-09-198-452A-121
US-08-551-437-2
US-09-004-225-2
US-09-084-346-2
US-09-004-346-2
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Best Local Similarity 100.
Matches 131; Conservative
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